Figure 1(A)

G***GATC***GTCTCAGGTCAGCGGAGGGA 25

SL33

GGAGACTTATAGACCTATCCAGTCT 50
TCAAGGTGCTCCAGAAAGCAGGAGT 75
TGAAGACCTGGGTGTGAGGGACACA 100
TACATCCTAAAAGCACCACAGCAGA 125
GGAGGCCCAGGCAGTGCCAGGAGTC 150
AAGGTTCCCAGAAGACAAACCCCCT 175
AGGAAGACAGGCGACCTGTGAGGCC 200
CTAGAGCACCACCTTAAGAGAAGAA 225

SL34

GAGCTGTAAGCCGGCCTTTGTCAGA 250
GCCATC**ATG**GGGGACAAGGATATGC 275
CTACTGCTGGGATGCCGAGTCTTCT 300
CCAGAGTTCCTCTGAGAGTCCTCAG 325
AGTTGTCCTGAGGGGGAGGACTCCC 350
AGTCTCCTCTCCAGATTCCCCAGAG 375
TTCTCCTGAGAGCGACGACACCCTG 400
TATCCTCTCCAGAGTCCTCAGAGTC 425
GTTCTGAGGGGGAGGACTCCTCG**GA** 450
TCCTCTCCAGAGACCTCCTGAGGGG 475
AAGGACTCCCAGTCTCCTCTCCAGA 500
TTCCCCAGAGTTCTCCTGAGGGCGA 525
CGACACCCAGTCTCCTCTCCAGAAT 550
TCTCAGAGTTCTCCTGAGGGGAAGG 575
ACTCCCTGTCTCCTCTAGAGATTTC 600
TCAGAGCCCTCCTGAGGGTGAGGAT 625
GTCCAGTCTCCTCTGCAGAATCCTG 650
CGAGTTCCTTCTTCTCCTCTGCTTT 675
ATTGAGTATTTTCCAGAGTTCCCCT 700

Figure 1(B)

```
GAGAGAACTCAGAGTACTTTTGAGG    725
GTTTTCCCCAGTCTCCTCTCCAGAT    750
TCCTGTGAGCTCCTCCTCCTCCTCC    775
ACTTTATTGAGTCTTTTCCAGAGTT    800
CCCCTGAGAGAACTCAGAGTACTTT    825
TGAGGGTTTTCCCCAGTCTCTTCTC    850
CAGATTCCTATGACCTCCTCCTTCT    875
CCTCTACTTTATTGAGTATTTTCCA    900
GAGTTCTCCTGAGAGTGCTCAAAGT    925
ACTTTTGAGGGTTTTCCCCAGTCTC    950
CTCTCCAGATTCCTGGGAGCCCCTC    975
CTTCTCCTCCACTTTACTGAGTCTT    1000
TTCCAGAGTTCCCCTGAGAGAACTC    1025
ACAGTACTTTTGAGGGTTTTCCCCA    1050
GTCTCCTCTCCAGATTCCTATGACC    1075
TCCTCCTTCTCCTCTACTTTATTGA    1100
GTATTTTCCAGAGTTCTCCTGAGAG    1125
TGCTCAAAGTACTTTTGAGGGTTTT    1150
CCCCAGTCTCCTCTCCAGATTCCTG    1175
GGAGCCCCTCCTTCTCCTCCACTTT    1200
ACTGAGTCTTTTCCAGAGTTCCCCT    1225
GAGAGAACTCACAGTACTTTTGAGG    1250
GTTTTCCCCAGTCTCCTCTCCAGAT    1275
TCCTATGACCTCCTCCTTCTCCTCT    1300
ACTTTATTGAGTATTTTACAGAGTT    1325
CTCCTGAGAGTGCTCAAAGTGCTTT    1350
TGAGGGTTTTCCCCAGTCTCCTCTC    1375
CAGATTCCTGTGAGCTCCTCTTTCT    1400
```

Figure 1(C)

CCTACACTTTATTGAGTCTTTTCCA	1425
GAGTTCCCCTGAGAGAACTCAGAGT	1450
ACTTTTGAGGGTTTTCCCCAGTCTC	1475
CTCTCCAGATTCCTGTGAGCTCCTC	1500
CTCCTCCTCCTCCACTTTATTGAGT	1525
CTTTTCCAGAGTTCCCCTGAGTGTA	1550
CTCAAAGTACTTTTGAGGGTTTTCC	1575
CCAGTCTCCTCTCCAGATTCCTCAG	1600
AGTCCTCCTGAAGGGGAGAATACCC	1625
ATTCTCCTCTCCAGATTGTTCCAAG	1650
TCTTCCTGAGTGGGAGGACTCCCTG	1675
TCTCCTCACTACTTTCCTCAGAGCC	1700
CTCCTCAGGGGGAGGACTCCCTATC	1725
TCCTCACTACTTTCCTCAGAGCCCT	1750
CCTCAGGGGGAGGACTCCCTGTCTC	1775
CTCACTACTTTCCTCAGAGCCCTCA	1800
GGGGGAGGACTCCCTGTCTCCTCAC	1825
TACTTTCCTCAGAGCCCTCCTCAGG	1850
GGGAGGACTCCATGTCTCCTCTCTA	1875
CTTTCCTCAGAGTCCTCTTCAGGGG	1900
GAGGAATTCCAGTCTTCTCTCCAGA	1925
GCCCTGTGAGCATCTGCTCCTCCTC	1950
CACTCCATCCAGTCTTCCCCAGAGT	1975
TTCCCTGAGAGTTCTCAGAGTCCTC	2000
CTGAGGGGCCTGTCCAGTCTCCTCT	2025
CCATAGTCCTCAGAGCCCTCCTGAG	2050
GGGATGCACTCCCAATCTCCTCTCC	2075
AGAGTCCTGAGAGTGCTCCTGAGGG	2100

Figure 1(D)

GGAGGATTCCCTGTCTCCTCTCCAA 2125
ATTCCTCAGAGTCCTCTTGAGGGAG 2150
AGGACTCCCTGTCTTCTCTCCATTT 2175
TCCTCAGAGTCCTCCTGAGTGGGAG 2200
GACTCCCTCTCTCCTCTCCACTTTC 2225
CTCAGTTTCCTCCTCAGGGGGAGGA 2250
CTTCCAGTCTTCTCTCCAGAGTCCT 2275
GTGAGTATCTGCTCCTCCTCCACTT 2300
CTTTGAGTCTTCCCCAGAGTTTCCC 2325
TGAGAGTCCTCAGAGTCCTCCTGAG 2350
GGGCCTGCTCAGTCTCCTCTCCAGA 2375
GACCTGTCAGCTCCTTCTTCTCCTA 2400
CACTTTAGCGAGTCTTCTCCAAAGT 2425
TCCCATGAGAGTCCTCAGAGTCCTC 2450
CTGAGGGGCCTGCCCAGTCTCCTCT 2475
CCAGAGTCCTGTGAGCTCCTTCCCC 2500
TCCTCCACTTCATCGAGTCTTTCCC 2525
AGAGTTCTCCTGTGAGCTCCTTCCC 2550
CTCCTCCACTTCATCGAGTCTTTCC 2575
AAGAGTTCCCCTGAGAGTCCTCTCC 2600
AGAGTCCTGT**GATC**TCCTTCTCCTC 2625
CTCCACTTCATTGAGCCCATTCAGT 2650
GAAGAGTCCAGCAGC<u>CCAGTAGATG</u> 2675
SL26
<u>AATATACAAGTT</u>CCTCAGACACCTT 2700
GCTAGAGAGTGATTCCTTGACAGAC 2725
AGCGAGTCCTTGATAGAGAGCGAGC 2750
CCTTGTTCACTTATACACTGGATGA 2775
AAAGGTGGACGAGTTGGCGCGGTTT 2800

Figure 1(E)

CTTCTCCTCAAATATCAAGTGAAGC	2825
SL27	
AGCCTATCACAAAGGCAGAGATGCT	2850
GACGAATGTCATCAGCAGGTACACG	2875
GGCTACTTTCCTGT***GATC***TTCAGGA	2900
AAGCCCGTGAGTTCATAGAGATACT	2925
TTTTGGCATTTCCCTGAGAGAAGTG	2950
GACCCTGATGACTCCTATGTCTTTG	2975
TAAACACATTAGACCTCACCTCTGA	3000
GGGGTGTCTGAGTGATGAGCAGGGC	3025
ATGTCCCAGAACCGCCTCCTGATTC	3050
TTATTCTGAGTATCATCTTCATAAA	3075
GGGCACCTATGCCTCTGAGGAGGTC	3100
ATCTGGGATGTGCTGAGTGGAATAG	3125
GGGTGCGTGCTGGGAGGGAGCACTT	3150
TGCCTTTGGGGAGCCCAGGGAGCTC	3175
CTCACTAAAGTTTGGGTGCAGGAAC	3200
ATTACCTAGAGTACCGGGAGGTGCC	3225
CAACTCTTCTCCTCCTCGTTACGAA	3250
TTCCTGTGGGGTCCAAGAGCTCATT	3275
CAGAAGTCATTAAGAGGAAAGTAGT	3300
AGAGTTTTTGGCCATGCTAAAGAAT	3325
ACCGTCCCTATTACCTTTCCATCCT	3350
CTTACAAGGATGCTTTGAAAGATGT	3375
GGAAGAGAGAGCCCAGGCCATAATT	3400
GACACCACAGATGATTCGACTGCCA	3425
CAGAAAGTGCAAGCTCCAGTGTCAT	3450
GTCCCCCAGCTTCTCTTC**TGA**GTGA	3475
AGTCTAGGGCAGATTCTTCCCTCTG	3500

Figure 1(F)

AGTTTGAAGGGGGCAGTCGAGTTTC	3525
TACGTGGTGGAGGGCCTGGTTGAGG	3550
CTGGAGAGAACACAGTGCTATTTGC	3575
ATTTCTGTTCCATATGGGTAGTTAT	3600
GGGGTTTACCTGTTTTACTTTTGGG	3625
TATTTTTCAAATGCTTTTCCTATTA	3650
ATAACAGGTTTAAATAGCTTCAGAA	3675
TCCTAGTTTATGCACATGAGTCGCA	3700
CATGTATTGCTGTTTTTCTGGTTTA	3725
AGAGTAACAGTTTGATATTTTGTAA	3750
AAACAAAAACACACCCAAACACACC	3775
ACATTGGGAAAACCTTCTGCCTCAT	3800
TTTGTGATGTGTCACAGGTTAATGT	3825
GGTGTTACTGTAGGAATTTTCTTGA	3850
AACTGTGAAGGAACTCTGCAGTTAA	3875
ATAGTGGAATAAAGTAAAGGATTGT	3900
TAATGTTTGCATTTCCTCAGGTCCT	3925
TTAGTCTGTTGTTCTTGAAAACTAA	3950
AGATACATACCTGGTTTGCTTGGCT	3975
TACGTAAGAAAGTAGAAGAAAGTAA	4000
ACTGTAATAAATAAAAAAAAAAAAA	4025
AAAAAA	4031

FIG. 2(A)

```
                                                                      exon I | intron I
exon I
CCATTCTGAGGGACGGCGTA  GAGTTCGGCCGAAGGAACCT  GACCCAGGCTCTGTGAGGAG  GCAAG|gtgag//.......  .......................   
..............................................................  .......  GGATCGT  CTCAGGTCAGCGGAGGGAGG   27
                                                                                  exon I

                            ..................//ctg  gagctccaggaaccaggcag  tgaggccttggt-------c  tgagacagtatcctcaggtc
......................  ..................  GTGCTCCAGAAAGCAGGAGT  TGAAGACCTGGGTGTGAGGG  ACACATACATCCTAAAAGCA   115
AGACTTATAGACCTATCCAG  TCTTCAAG|gt//...//cag
                         exon I |  intron I   exon II

acagagcagaggatgcacag  ggtgtgccagcagtgaatgt  tt------gccctgaatgca  caccaagggccccacctgcc  acaggacacataggactcca
CCACAGCAGAGGAGGCCCAG  GCAGTGCCAGGAGTCAAG|gt  gagtgcacgacctgactgtg  taccaagggccgtacccca  gaaacagtgtcagacctggc
                                 exon II | intron II                                            intron I | exon II
cagagtctggcctcacctcc  ctactgtcagtcctgtagaa  tcgac-ctctgctggccggc  tgtaccctga-gtaccctct  cacttcctccttcag|GTTTT   70
agcaccggccctgtagccac  ccactgtcattcctggtgcc  tcatggctctgcctgccagc  tgtgccccgaggtgctttct  cgcgtccttctacag|GTTCC  158
                                                                                                intron II | exon III
                                                                          exon II | intron II
CAGGGGACAGGCCAACCCAG  AGGACAGGATTCCCTGGAGG  CCACAGAGGAGCACC----A  AGGAGAAGATCT|gtaagtag  gcctttgttagagtctccaa
CAGAAGACAAACCCCCTAGG  AAGACAGGCGACCTGTGAGG  CCCTAGAGCACCACCTTAAG  AGAAGAAGAGCTGTAAGCCG  GCCTTTGTCAGAGCCATCAT   258
                                                                                                        M     1

                                                        intron II | exon III
                                              ctccc-cag|GCCTGTGGGTC  TTCATTG-CCCAGCTCCTGC  CCACACTCCTGCCTGCTGCC   188
ggttcag-ttctcagctgag  gcctctcacacactccctct  ctccctcagtcctgtgggat  cccatcatacctattcgtgt  tcacacgtttacctgctgct
GG|gtgagtttctcagctgag  gccactggcactgtccctct
on III G | intron III

                              M    S  L  E  Q  R  S  L    H  C  K  P  E  E  A   L  E  A  Q  Q  E    A  L  G  L  V  C  V    28
1  CT--GACGAGAGTCATCATG  TCTCTTGAGCAGAGGAGTCT  GCACTGCAAGCCTGAGGAAG  CCCTTGAGGCCCAACAAGAG  GCCCTGGGCCTGGTGTGTGT  286
1  cctgaacaatattcatcatg  cctctctttctaaaccttcc  acgccccagctttgagcaag  gcttccagaaggcaattttc  atactggagttggtagatgc

   Q  A  A  T  S  S  S    S  P  L  V  L  G    T  L  E  E  V  P  T    A  G  S  T  D  P  P    Q  S  P  Q  G  A    61
1  GCAGGCTGCCACCTCCTCCT  CCTCTCCTCTGGTCCTGGGC  ACCCTGGAGGAGGTGCCCAC  TGCTGGGTCAACAGATCCTC  CCCAGAGTCCTCAGGGAGCC  386
1  agaggatccccca-------  ....................  ....................  ....................  ....................

                                                                                                               76
   S  A  F  P  T  T  I    N  F  T  R  Q  R  Q    P                                                          431
1  TCCGCCTTTCCCACTACCAT  CAACTTCACTCGACAGAGGC  AACCC...............  ....................  ....................
1  ....................  ....................  .....gatgaggaagaggag  gaagcttcctccatttctc  ttcctctttccactttttat
```

FIG. 2(B)

```
tccccicgtcctcctcctgt ttttctttctcatcctcatc ctcctctctgcttctgcgtt ctccag|GGGACAAGGATATG  CCTACTGCTGGGATGCCGAG  294
                                                           intron III|   D  K  D  M    P  T  A  G  M  P  S    13
                                                                        exon IV

TCTTCTCCAGAGTTCCTCTG  AGAGTCCTCAGAGTTGTCCT  GAGGGGGAGGACTCCCAGTC  TCCTCTCCAGATTCCCCAGA  GTTCTCCTGAGAGCGACGAC  394
 L  L  Q  S  S  S  E    S  P  Q  S |Y  P    E  G  E  D  S  Q  S    P  L  Q  I  P|| Q  S    S  P  E  S  D  D    46

ACCCTGTATCCTCTCCAGAG  TCCTCAGAGTCGTTCTGAGG  GGGAGGACTCCTCGGATCCT  CTCCAGAGACCTCCTGAGGG  GAAGGACTCCCAGTCTCCTC  494
 T  L  Y  P  L  Q  S    P||Q  S  R  S  E  G    E  D  S  S  D  P    L  Q  R||P  P  E  G    K  D  S  Q  S  P  L    80

TCCAGATTCCCCAGAGTTCT  CCTGAGGGCGACGACACCCA  GTCTCCTCTCCAGAATTCTC  AGAGTTCTCCTGAGGGGAAG  GACTCCCTGTCTCCTCTAGA  594
 Q  I  P||Q  S  S    P  E  G  D  D  T  Q    S  P  L  Q  N  S||Q    S  S  P  E  G  K    D  S  L  S  P  L  E    113

GATTTCTCAGAGCCCTCCTG  AGGGTGAGGATGTCCAGTCT  CCTCTGCAGAATCCTGCGAG  TTCCTTCTTCTCCTCTGCTT  TATTGAGTATTTTCCAGAGT  694
 I  S||Q  S  P  P  E    G  E  D  V  Q  S    P  L  Q  N  P||A  S    S  F  F  S  S  A  L    L  S  I  F  Q  S    146

TCCCCTGAGAGTATTCAAAG  TCCTTTTGAGGGTTTTCCCC  AGTCTGTTCTCCAGATTCCT  GTGAGCGCCGCCTCCTCCTC  CACTTTAGTGAGTATTTTCC  794
 S  P  E  S  I  Q||S    P  F  E  G  F  P  Q    S  V  L  Q  I  P|  |V  S  A  A  S  S  S    T  L  V  S  I  F  Q    180

AGAGTTCCCCTGAGAGTACT  CAAAGTCCTTTTGAGGGTTT  TCCCCAGTCTCCACTCCAGA  TTCCTGTGAGCCGCTCCTTC  TCCTCCACTTTATTGAGTAT  894
 S  S  P  E  S  T    Q||S  P  F  E  G  F    P  Q  S  P  L  Q  I    P||V  S  R  S  F    S  S  T  L  L  S  I    213

TTTCCAGAGTTCCCCTGAGA  GAAGTCAGAGAACTTCTGAG  GGTTTTGCACAGTCTCCTCT  CCAGATTCCTGTGAGCTCCT  CCTCGTCCTCCACTTTACTG  994
 F  Q  S  S  P  E  R    S  Q||R  T  S  E    G  F  A  Q  S  P  L    Q  I  P||V  S  S  S    S  S  S  T  L  L    246
```

FIG. 2(C)

```
A1  .................... .................... .................... .................... ....................
C1  AGTCTTTTCCAGAGTTCCCC TGAGAGAACTCAGAGTACTT TTGAGGGTTTTCCCCAGTCT CCACTCCAGATTCCTGTGAG CCGCTCCTTCTCCTCCACTT 1094
     S L F Q S S P  E R T Q | S T F  E G F P Q S  P L Q I P | V S  R S F S S T L  280

A1  .................... .................... .................... .................... ....................
C1  TATTGAGTATTTTCCAGAGT TCCCCTGAGAGAACTCAGAG TACTTTTGAGGGTTTTGCCC AGTCTCCTCTCCAGATTCCT GTGAGCTCCTCCTCCTCCTC 1194
     L S I F Q S  S P E R T Q | S  T F E G F A Q  S P L Q I P | V S S S S S S  313

A1  .................... .................... .................... .................... ....................
C1  CACTTTATTGAGTCTTTTCC AGAGTTCCCCTGAGAGAACT CAGAGTACTTTTGAGGGTTT TCCCCAGTCTCTTCTCCAGA TTCCTATGACCTCCTCCTTC 1294
     T L L S L F Q  S S P E R T  Q | S T F E G F  P Q S L L Q I  P | M T S S F  346

A1  .................... .................... .................... .................... ....................
C1  TCCTCTACTTTATTGAGTAT TTTCCAGAGTTCTCCTGAGA GTGCTCAAAGTACTTTTGAG GGTTTTCCCCAGTCTCCTCT CCAGATTCCTGGGAGCCCCT 1394
     S S T L L S I  F Q S S P E S  A Q | S T F E  G F P Q S P L  Q I P | G S P S  380

A1  .................... .................... .................... .................... ....................
C1  CCTTCTCCTCCACTTTACTG AGTCTTTTCCAGAGTTCCCC TGAGAGAACTCACAGTACTT TTGAGGGTTTTCCCCAGTCT CCTCTCCAGATTCCTATGAC 1494
     F S S T L L  S L F Q S S P  E R T H | S T F  E G F P Q S  P L Q I P | M T  413

A1  .................... .................... .................... .................... ....................
C1  CTCCTCCTTCTCCTCTACTT TATTGAGTATTTTACAGAGT TCTCCTGAGAGTGCTCAAAG TGCTTTTGAGGGTTTTCCCC AGTCTCCTCTCCAGATTCCT 1594
     S S F S S T L  L S I L Q S  S P E S A Q | S  A F E G F P Q  S P L Q I P |  446

A1  .................... .................... .................... .................... ....................
C1  GTGAGCTCCTCTTTCTCCTA CACTTTATTGAGTCTTTTCC AGAGTTCCCCTGAGAGAACT CAGAGTACTTTTGAGGGTTT TCCCCAGTCTCCTCTCCAGA 1694
    | V S S S F S Y  T L L S L F Q  S S P E R T  Q | S T F E G F  P Q S P L Q I  480

A1  .................... .................... .................... .................... ....................
C1  TTCCTGTGAGCTCCTCCTCC TCCTCCTCCACTTTATTGAG TCTTTTCCAGAGTTCCCCTG AGTGTACTCAAAGTACTTTT GAGGGTTTTCCCCAGTCTCC 1794
     P | V S S S S  S S S T L L S  L F Q S S P E  C T Q | S T F  E G F P Q S P  513
```

FIG. 2(D)

```
A1 ..........................................................................................................
C1 TCTCCAGATTCCTCAGAGTC CTCCTGAAGGGGAGAATACC CATTCTCCTCTCCAGATTGT TCCAAGTCTTCCTGAGTGGG AGGACTCCCTGTCTCCTCAC 1894
    L  Q  I  P  Q  S  P   P  E  G  E  N  T   H  S  P  L  Q  I  V   P  S  L  P  E  W  E   D  S  L  S  P  H   546

A1 ..........................................................................................................
C1 TACTTTCCTCAGAGCCCTCC TCAGGGGGAGGACTCCCTAT CTCCTCACTACTTTCCTCAG AGCCCTCCTCAGGGGGAGGA CTCCCTGTCTCCTCACTACT 1994
    Y  F  P  Q  S  P  P   Q  G  E  D  S  L  S   P  H  Y  F  P  Q   S  P  P  Q  G  E  D   S  L  S  P  H  Y  F  580

A1 ..........................................................................................................
C1 TTCCTCAGAGCCCTCAGGGG GAGGACTCCCTGTCTCCTCA CTACTTTCCTCAGAGCCCTC CTCAGGGGGAGGACTCCATG TCTCCTCTCTACTTTCCTCA 2094
    P  Q  S  P  Q  G   E  D  S  L  S  P  H   Y  F  P  Q  S  P  P   Q  G  E  D  S  M   S  P  L  Y  F  P  Q  613

A1 ..........................................................................................................
C1 GAGTCCTCTTCAGGGGGAGG AATTCCAGTCTTCTCTCCAG AGCCCTGTGAGCATCTGCTC CTCCTCCACTCCATCCAGTC TTCCCCAGAGTTTCCCTGAG 2194
    S  P  L  Q  G  E  E   F  Q  S  S  L  Q   S  P  V  S  I  C  S   S  S  T  P  S  S  L   P  Q  S  F  P  E  646

A1 ..........................................................................................................
C1 AGTTCTCAGAGTCCTCCTGA GGGGCCTGTCCAGTCTCCTC TCCATAGTCCTCAGAGCCCT CCTGAGGGGATGCACTCCCA ATCTCCTCTCCAGAGTCCTG 2294
    S  S  Q  S  P  P  E   G  P  V  Q  S  P  L   H  S  P  Q  S  P   P  E  G  M  H  S  Q   S  P  L  Q  S  P  E  680

A1 ..........................................................................................................
C1 AGAGTGCTCCTGAGGGGGAG GATTCCCTGTCTCCTCTCCA AATTCCTCAGAGTCCTCTTG AGGGAGAGGACTCCCTGTCT TCTCTCCATTTTCCTCAGAG 2394
    S  A  P  E  G  E   D  S  L  S  P  L  Q   I  P  Q  S  P  L  E   G  E  D  S  L  S   S  L  H  F  P  Q  S  713

A1 ..........................................................................................................
C1 TCCTCCTGAGTGGGAGGACT CCCTCTCTCCTCTCCACTTT CCTCAGTTTCCTCCTCAGGG GGAGGACTTCCAGTCTTCTC TCCAGAGTCCTGTGAGTATC 2494
    P  P  E  W  E  D  S   L  S  P  L  H  F   P  Q  F  P  P  Q  G   E  D  F  Q  S  S  L   Q  S  P  V  S  I  746

A1 ..........................................................................................................
C1 TGCTCCTCCTCCACTTCTTT GAGTCTTCCCCAGAGTTTCC CTGAGAGTCCTCAGAGTCCT CCTGAGGGGCCTGCTCAGTC TCCTCTCCAGAGACCTGTCA 2594
    C  S  S  S  T  S  L   S  L  P  Q  S  F  P   E  S  P  Q  S  P   P  E  G  P  A  Q  S   P  L  Q  R  P  V  S  780

A1 ..........................................................................................................
C1 GCTCCTTCTTCTCCTACACT TTAGCGAGTCTTCTCCAAAG TTCCCATGAGAGTCCTCAGA GTCCTCCTGAGGGGCCTGCC CAGTCTCCTCTCCAGAGTCC 2694
    S  F  F  S  Y  T   L  A  S  L  L  Q  S   S  H  E  S  P  Q  S   P  P  E  G  P  A   Q  S  P  L  Q  S  P  813
```

10085108.030102

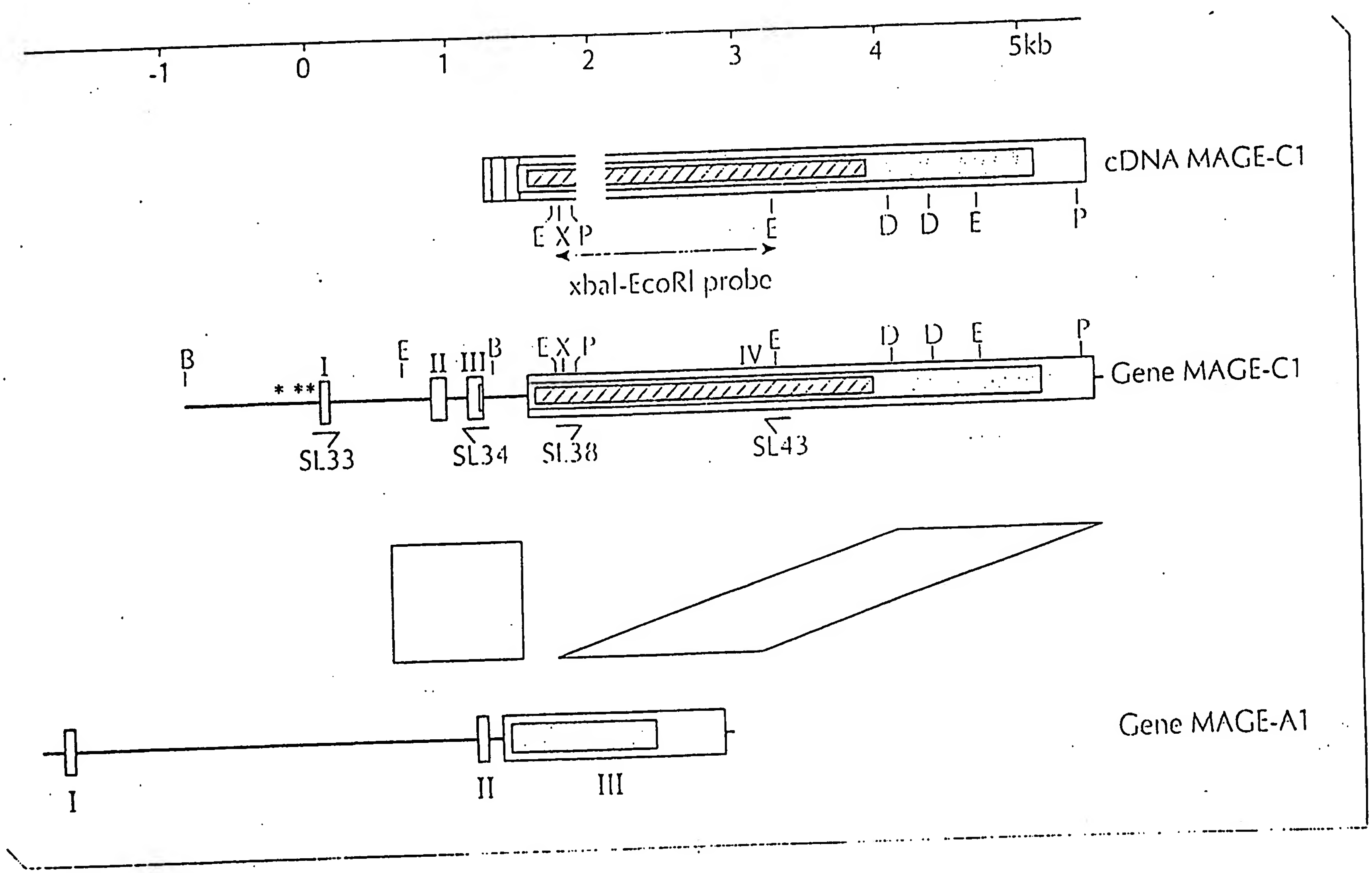
FIG. 2(E)

```
A1 ............................................................................................... 
C1 TGTGAGCTCCTTCCCCTCCT CCACTTCATCGAGTCTTTCC CAGAGTTCTCCTGTGAGCTC CTTCCCCTCCTCCACTTCAT CGAGTCTTTCCAAGAGTTCC 2794
    V  S  S  F  P  S  S   T  S  S  S  L  S   Q  S  S  P  V  S  S   F  P  S  S  T  S  S   S  L  S  K  S  S    846

                                                                  S  E  G  S  S  S   R  E  E  E  G  P  S    89
                                                               ...AGTGAGGGTTCCAGCAG CCGTGAAGAGGAGGGGCCAA  468
A1 .............................................................
C1 CCTGAGAGTCCTCTCCAGAG TCCTGTGATCTCCTTCTCCT CCTCCACTTCATTGAGCCCA TTCAGTGAAGAGTCCAGCAG CCCAGTAGATGAATATACAA 2894
    P  E  S  P  L  Q  S  P  V  I  S  F  S  S   S  T  S  L  S  P  S   S  E  E  S  S  S   P  V  D  E  Y  T  S    880

    T  S  C  I  L  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .   E  S  L  F  R  A   V  I  T  K  K  V  A   108
A1 GCACCTCTTGTATCCTG--- .......................................--GAGTCCTTGTTCCGAGCA GTAATCACTAAGAAGGTGGC  523
C1 GTTCCTCAGACACCTTGCTA GAGAGTGATTCCTTGACAGA CAGCGAGTCCTTGATAGAGA GCGAGCCCTTGTTCACTTAT ACACTGGATGAAAAGGTGGA 2994
    S  S  D  T  L  L   E  S  D  S  L  T  D   S  E  S  L  I  E  S   E  P  L  F  T  Y   T  L  D  E  K  V  D   913

    D  L  V  G  F  L  L   L  K  Y  R  A  R   E  P  V  T  K  A  E   M  L  E  S  V  I  K   N  Y  K  H  C  F   140
A1 TGATTTGGTTGGTTTTCTGC TCCTCAAATATCGAGCCAGG GAGCCAGTCACAAAGGCAGA AATGCTGGAGAGTGTCATCA AAAATTACAAGCACTGTTTT  623
C1 CGAGTTGGCGCGGTTTCTTC TCCTCAAATATCAAGTGAAG CAGCCTATCACAAAGGCAGA GATGCTGACGAATGTCATCA GCAGGTACACGGGCTACTTT 3094
    E  L  A  R  F  L  L   L  K  Y  Q  V  K   Q  P  I  T  K  A  E   M  L  T  N  V  I  S   R  Y  T  G  Y  F   946

    P  E  I  F  G  K  A   S  E  S  L  Q  L  V   F  G  I  D  V  K   E  A  D  P  T  G  H   S  Y  V  L  V  T  C   174
A1 CCTGAGATCTTCGGCAAAGC CTCTGAGTCCTTGCAGCTGG TCTTTGGCATTGACGTGAAG GAAGCAGACCCCACCGGCCA CTCCTATGTCCTTGTCACCT  723
C1 CCTGTGATCTTCAGGAAAGC CCGTGAGTTCATAGAGATAC TTTTTGGCATTTCCCTGAGA GAAGTGGACCCT---GATGA CTCCTATGTCTTTGTAAACA 3191
    P  V  I  F  R  K  A   R  E  F  I  E  I  L   F  G  I  S  L  R   E  V  D  P  -  D  D   S  Y  V  F  V  N  T   979

    L  G  L  S  Y  D   G  L  L  G  D  N  Q   I  M  P  K  T  G  F   L  I  I  V  L  V   M  I  A  M  E  G  G   207
A1 GCCTAGGTCTCTCCTATGAT GGCCTGCTGGGTGATAATCA GATCATGCCCAAGACAGGCT TCCTGATAATTGTCCTGGTC ATGATTGCAATGGAGGGCGG  823
C1 CATTAGACCTCACCTCTGAG GGGTGTCTGAGTGATGAGCA GGGCATGTCCCAGAACCGCC TCCTGATTCTTATTCTGAGT ATCATCTTCATAAAGGGCAC 3291
    L  D  L  T  S  E   G  C  L  S  D  E  Q   G  M  S  Q  N  R  L   L  I  L  I  L  S   I  I  F  I  K  G  T   1012

    H  A  P  E  E  E  I   W  E  E  L  S  F   M  E  V  Y  D  G  R   E  H  S  A  Y  G  E   P  R  K  L  L  T   240
A1 CCATGCTCCTGAGGAGGAAA TCTGGGAGGAGCTGAGTGTG ATGGAGGTGTATGATGGGAG GGAGCACAGTGCCTATGGGG AGCCCAGGAAGCTGCTCACC  923
C1 CTATGCCTCTGAGGAGGTCA TCTGGGATGTGCTGAGTGGA ATAGGGGTGCGTGCTGGGAG GGAGCACTTTGCCTTTGGGG AGCCCAGGGAGCTCCTCACT 3391
    Y  A  S  E  E  V  I   W  D  V  L  S  G   I  G  V  R  A  G  R   E  H  F  A  F  G  E   P  R  E  L  L  T   1045
```

FIG. 2(F)

```
Q D L V Q E K        Y L E Y R Q V        P D S D P A          R Y E F L W G        P R A L A E T        274
CAAGATTTGGTGCAGGAAAA GTACCTGGAGTACCGGCAGG TGCCGGACAGTGATCCCGCA CGCTATGAGTTCCTGTGGGG TCCAAGGGCCCTCGCTGAAA 1023
AAAGTTTGGGTGCAGGAACA TTACCTAGAGTACCGGGAGG TGCCCAACTCTTCTCCTCCT CGTTACGAATTCCTGTGGGG TCCAAGAGCTCATTCAGAAG 3491
K V W V Q E H        Y L E Y R E V        P N S S P P          R Y E F L W G        P R A H S E V        1079

 S Y V K V L         E Y V I K V S        A R V R F F F        P S L R E A          A L R E E E E        307
CCAGCTATGTGAAAGTCCTT GAGTATGTGATCAAGGTCAG TGCAAGAGTTCGCTTTTTCT TCCCATCCCTGCGTGAAGCA GCTTTGAGAGAGGAGGAAGA 1123
TCATTAAGAGGAAAGTAGTA GAGTTTTTGGCCATGCTAAA GAATACCGTCCCTATTACCT TTCCATCCTCTTACAAGGAT GCTTTGAAAGATGTGGAAGA 3591
 I K R K V V         E F L A M L K        N T V P I T F        P S S Y K D          A L K D V E E        1112

                                                                                                         309
G V OPA
GGGAGTCTGAGCATGAGTTG CAGCCAAGGCCAGTGGGAGG GGGACTGGGCCAGTGCACCT TCCAGGGCCGCGTCCAGCAG CTTCCCCTGCCTCGTGTGAC 1223
GAGAGCCCAGGCCATAATTG ACACCACAGATGATTCGACT GCCACAGAAAGTGCAAGCTC CAGTGTCATGTCCCCCAGCT TCTCTTCTGAGTGAAGTCTA 3691
R A Q A I I D        T T D D S T          A T E S A S S        S V M S P S F        S S E OPA            1142

---ATGAGGCCCATTCTTCA CTCTGAAGAGAGCGGTCAGT GTTCTCAGTAGTAG------ -------------------- ---------------GTTTC 1279
GGGCAGATTCTTCCCTCTGA GTTTGAAGGGGGCAGTCGAG TTTCTACGTGGTGGAGGGCC TGGTTGAGGCTGGAGAGAAC ACAGTGCTATTTGCATTTCT 3791

TGTTCTATTGGGTGACTTGG AGATTTATCTTTGTTCTCTT TTGGAATTGTTCAAATGTTT TT--TTTTAAGGGATGGTTG AATGAACTTCAGCATCCAAG 1377
GTTCCATATGGGTAGTTATG GGGTTTACCTGTTTTACTTT TGGGTATTTTTCAAATGCTT TTCCTATTAATAACAGGTTT AAATAGCTTCAGAATCCTAG 3891

TTTATGAATGACAGCAGT-C ACACAGTTCTGTGTATATAG TTTAAGGGTAAGAGTCTTGT GTTTTATTCAGATTGGGAAA TCCATTCTATTTTGTGAATT 1476
TTTATGCACATGAGTCGCAC ATGTATTGCTGTTTTTCTGG TTTAAGAGTAACAGTTTGAT ATTTTGTAAAAACAAAAACA CACCCAAACACACCACATTG 3991

GGGATAATAACAGCAGTGGA ATAAGTACTTAGAATGTGA  AAAATGAGCAGTAAAATAGA TGAGATAAAGAACTAAAGAA ATTAAGAGATAGTCAATTCT 1576
GGAAAACCTTCTGCCTCATT TTGTGATGTGTCACAGGTTA ATGTGGTGTTACTGTAGGAA TTTTCTTGAAACTGTGAAGG AACTCTGCAGTTAAATAGTG 4091

TGCCTTATACCTCAGTCTAT TCTGTAAAATTTTTAAAGAT ATATGCATACCTGGATTTCC TTGGCTTCTTTGAGAATGTA AGAGAAATTAAATCTGAATA 1676
GAATAAAGTAAAGGATTGTT AATGTTTGCATTTCCTCAGG TCCTTTAGTCTGTTGTTCTT GAAAACTAAAGATACATACC TGGTTTGCTTGGCTTACGTA 4191

                                                                                                         1691
AAGAATTCTTCCTGT----- --------------                                                                      4225
AGAAAGTAGAAGAAAGTAAA CTGTAATAAATAAA
```

FIG. 3


-1
0
1
2
3
4
5kb
cDNA MAGE-C1
E X P
E
D D E
P
xbal-EcoRI probe
Gene MAGE-C1
B
* **
I
E
II
III
B
E X P
IV
E
D D E
P
SL33
SL34
SL38
SL43
Gene MAGE-A1
I
II
III

10065108.030102

FIG. 4

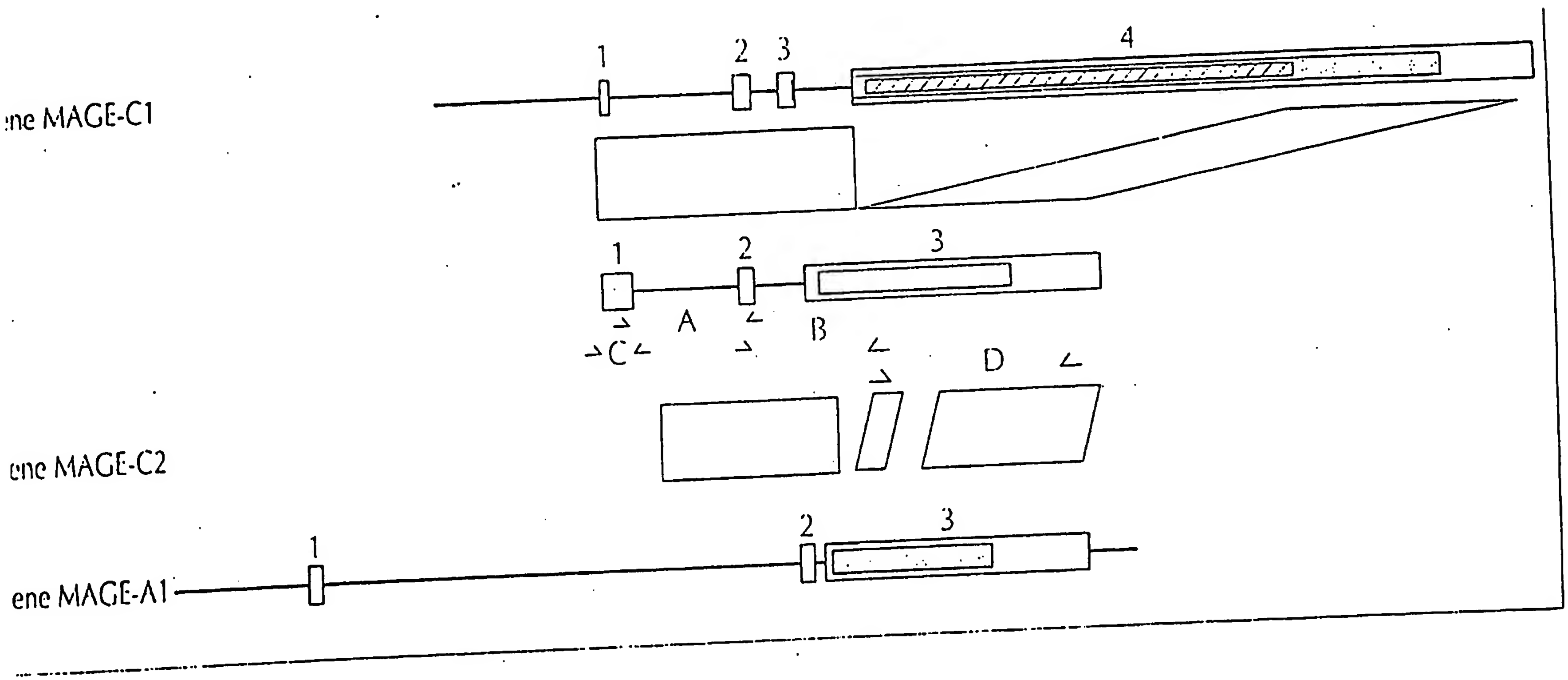


Figure 5 **Nucleotide sequence of gene MAGE-C3 (SEQ ID NO: 21)**

The sequence corresponds to nucleotides 3761 to 4801 of PAC clone 232G24 (GenBank accession number AL022152). It has been renumbered in this figure, taking as nucleotide number 1 the first nucleotide of the start codon.

Primers SL164 and SL165 that were used in the RT-PCR assay are indicated.

ATGCCTCTCTTTCCAAACCTTCCACGCCTCAGCTTTGAGGAAGACTTCCA	50
GAACCCGAGTGTGACAGAGGACTTGGTAGATGCACAGGATTCCATAGATG	100
AGGAGGAGGAGGATGCCTCCTCCACTTCCTCTTCCTCTTTCCACTTTTTA	150
TTCCCCTCCTCCTCTTCCTTGTCC<u>TCATCCTCACCCTTGTCCTCA</u>CCCTT	200
SL164	
ACCCTCTACTCTCATTCTGGGTGTTCCAGAAGATGAGGATATGCCTGCTG	250
CTGGGATGCCACCTCTTCCCCAGAGTCCTCCTGAGATTCCTCCCCAGGGT	300
CCTCCCAAGATCTCTCCCCAGGGTCCTCCGCAGAGTCCTCCCCAGAGTCC	350
TCTAGACTCCTGCTCATCCCCTCTTTTGTGGACCCGATTGGATGAGGAGT	400
CCAGCAGTGAAGAGGAGGATACAGCTACTTGGCATGCCTTGCCAGAAAGT	450
GAATCCTTGCCCAGGTATGCCCTGGATGAAAAGGTGGCTGAGTTGGTGCA	500
GTTTCTTCTCCTCAAATATCAAACAAAAGAGCCTGTCACAAAGGCAGAGA	550
TGCTGACGACTGTCATCAAGAAGTATAAGGACTATTTTCCCATGATCTTC	600
GGGAAAGCCCATGAGTTCATAGAGCTAATTTTTGGCATTGCCCTGACTGA	650
TATGGACCCCGACAACCACTCCTATTTCTTTGAAGACACATTAGACCTCA	700
CCTATGAGGG<u>AAGCCTGATTGATGACCAGGG</u>CATGCCCAAGAACTGTCTC	750
SL165	
CTGATTCTTATTCTCAGTATGATCTTCATAAAGGGCAGCTGTGTCCCCGA	800
GGAGGTCATCTGGGAAGTGTTGAGTGCAATAGGGGTGTGTGCTGGGAGGG	850
AGCACTTTATATATGGGGATCCCAGAAAGCTGCTCACTATACATTGGGTG	900
CAGAGAAAGTACCTGGAGTACCGGGAGGTGCCCAACAGTGCTCCTCCACG	950
TTATGAATTTTTGTGGGGTCCAAGAGCCCATTCAGAGGCCAGCAAGAGAA	1000
GTCTTAGAGTTTTTATCCAAGCTATCCAGTATCATCCCTAG	1041

Figure 6 **Amino-acid sequence of the putative MAGE-C3 protein (SEQ ID NO: 22)**

MPLFPNLPRLSFEEDFQNPSVTEDLVDAQDSIDEEEEDASSTSSSSFHFL	50
FPSSSSLSSSSPLSSPLPSTLILGVPEDEDMPAAGMPPLPQSPPEIPPQG	100
PPKISPQGPPQSPPQSPLDSCSSPLLWTRLDEESSSEEEDTATWHALPES	150
ESLPRYALDEKVAELVQFLLLKYQTKEPVTKAEMLTTVIKKYKDYFPMIF	200
GKAHEFIELIFGIALTDMDPDNHSYFFEDTLDLTYEGSLIDDQGMPKNCL	250
LILILSMIFIKGSCVPEEVIWEVLSAIGVCAGREHFIYGDPRKLLTIHWV	300
QRKYLEYREVPNSAPPRYEFLWGPRAHSEASKRSLRVFIQAIQYHP	346

Figure 7 **Nucleotide sequence of gene MAGE-B5 (SEQ ID NO: 23)**

This sequence is the antiparallel sequence corresponding to nucleotides 123358 to 124185 of BAC clone 466O4 (GenBank accession number AC005297). The sequence has been renumbered in this figure, taking the first nucleotide of the start codon as nucleotide number 1.

Primers SL189 and SL190 that were used in the RT-PCR assay are indicated.

```
ATGACTTCTGCAGGTGTTTTTAATGCAGGATCTGACGAAAGGGCTAACAG     50
TAGAGATGAGGAGTACCCATGTTCCTCAGAGGTCTCACCCTCCACTGAGA    100
GTTCATGCAGCAATTTCATAAATATTAAGGTGGGTTTGTTGGAGCAGTTC    150
CTGCTCTACAAGTTCAAAATGAAACAGCGTATTTTGAAGGAAGATATGCT    200
GAAGATTGTCAACCCAAGATACCAAAACCAGTTTGCTGAGATTCACAGAA    250
GAGCTTCTGAGCACATTGAGGTTGTCTTTGCAGTTGACTTGAAGGAAGTC    300
AACCCAACTTGTCACTTATATGACCTTGTCAGCAAGCTGAAACTCCCCAA    350
CAATGGGAGGATTCATGTTGGCAAAGTGTTACCCAAGACTGGTCTCCTCA    400
                                  SL189
TGACTTTCCTGGTTGTGATCTTCCTGAAAGGCAACTGTGCCAACAAGGAA    450
GATACCTGGAAATTTCTGGATATGATGCAAATATATGATGGGAAGAAGTA    500
CTACATCTATGGAGAGCCCAGGAAGCTCATCACTCAGGATTTCGTGAGGC    550
TAACGTACCTGGAGTACCACCAGGTGCCCTGCAGTTATCCTGCACACTAT    600
CAATTCCTTTGGGGTCCAAGAGCCTATACTGAAACCAGCAAGATGAAAGT    650
CCTGGAATATTTGGCCAAGGTCAATGATATTGCTCCAGGTGCCTTCTCAT    700
                                         SL190
CACAATATGAAGAGGCTTTGCAAGATGAGGAAGAGAGCCCAAGCCAGAGA    750
TGCAGCCGAAACTGGCACTACTGCAGTGGCCAAGACTGTCTCAGGGCGAA    800
GTTCAGCAGCTTCTCTCAACCCTATTGA                          828
```

Figure 8 **Amino-acid sequence of the putative MAGE-B5 protein (SEQ ID NO: 24)**

MTSAGVFNAGSDERANSRDEEYPCSSEVSPSTESSCSNFINIKVGLLEQF 50
LLYKFKMKQRILKEDMLKIVNPRYQNQFAEIHRRASEHIEVVFAVDLKEV 100
NPTCHLYDLVSKLKLPNNGRIHVGKVLPKTGLLMTFLVVIFLKGNCANKE 150
DTWKFLDMMQIYDGKKYYIYGEPRKLITQDFVRLTYLEYHQVPCSYPAHY 200
QFLWGPRAYTETSKMKVLEYLAKVNDIAPGAFSSQYEEALQDEEESPSQR 250
CSRNWHYCSGQDCLRAKFSSFSQPY 275

Figure 9 **Nucleotide sequence of gene MAGE-B6 (SEQ ID NO: 25)**

This sequence is the antiparallel sequence corresponding to nucleotides 146417 to 147640 of BAC clone 466O4 (GenBank accession number AC005297). The sequence has been renumbered in this figure, taking the first nucleotide of the start codon as nucleotide number 1.

Primers SL191 and SL192 that were used in the RT-PCR assay are indicated.

```
ATGCCTCGGGGTCACAAGAGTAAGCTCCGTACCTGTGAGAAACGCCAAGA    50
GACCAATGGTCAGCCACAGGGTCTCACGGGTCCCCAGGCCACTGCAGAGA    100
AGCAGGAAGAGTCCCACTCTTCCTCATCCTCTTCTCGCGCTTGTCTGGGT    150
                          SL191
GATTGTCGTAGGTCTTCTGATGCCTCCATTCCTCAGGAGTCTCAGGGAGT    200
GTCACCCACTGGGTCTCCTGATGCAGTTGTTTCATATTCAAAATCCGATG    250
TGGCTGCCAACGGCCAAGATGAGAAAAGTCCAAGCACCTCCCGTGATGCC    300
TCCGTTCCTCAGGAGTCTCAGGGAGCTTCACCCACTGGCTCTCCTGATGC    350
AGGTGTTTCAGGCTCAAAATATGATGTGGCTGCCAACGGCCAAGATGAGA    400
AAAGTCCAAGCACTTCCCATGATGTCTCCGTTCCTCAGGAGTCTCAGGGA    450
GCTTCACCCACTGGCTCGCCTGATGCAGGTGTTTCAGGCTCAAAATATGA    500
TGTGGCTGCCGAGGGTGAAGATGAGGAAAGTGTAAGCGCCTCACAGAAAG    550
                SL192
CCATCATTTTTAAGCGCTTAAGCAAAGATGCTGTAAAGAAGAAGGCGTGC    600
ACGTTGGCGCAATTCCTGCAGAAGAAGTTTGAGAAGAAAGAGTCCATTTT    650
GAAGGCAGACATGCTGAAGTGTGTCCGCAGAGAGTACAAGCCCTACTTCC    700
CTCAGATCCTCAACAGAACCTCCCAACATTTGGTGGTGGCCTTTGGCGTT    750
GAATTGAAAGAAATGGATTCCAGCGGCGAGTCCTACACCCTTGTCAGCAA    800
GCTAGGCCTCCCCAGTGAAGGAATTCTGAGTGGTGATAATGCGCTGCCGA    850
AGTCGGGTCTCCTGATGTCGCTCCTGGTTGTGATCTTCATGAACGGCAAC    900
TGTGCCACTGAAGAGGAGGTCTGGGAGTTCCTGGGTCTGTTGGGGATATA    950
TGATGGGATCCTGCATTCAATCTATGGGGATGCTCGGAAGATCATTACTG    1000
AAGATTTGGTGCAAGATAAGTACGTGGTTTACCGGCAGGTGTGCAACAGT    1050
GATCCTCCATGCTATGAGTTCCTGTGGGGTCCACGAGCCTATGCTGAAAC    1100
CACCAAGATGAGAGTCCTGCGTGTTTTGGCCGACAGCAGTAACACCAGTC    1150
CCGGTTTATACCCACATCTGTATGAAGACGCTTTGATAGATGAGGTAGAG    1200
AGAGCATTGAGACTGAGAGCTTAA                              1224
```

Figure 10 **Amino-acid sequence of the putative MAGE-B6 protein (SEQ ID NO: 26)**

```
MPRGHKSKLRTCEKRQETNGQPQGLTGPQATAEKQEESHSSSSSSRACLG   50
DCRRSSDASIPQESQGVSPTGSPDAVVSYSKSDVAANGQDEKSPSTSRDA  100
SVPQESQGASPTGSPDAGVSGSKYDVAANGQDEKSPSTSHDVSVPQESQG  150
ASPTGSPDAGVSGSKYDVAAEGEDEESVSASQKAIIFKRLSKDAVKKKAC  200
TLAQFLQKKFEKKESILKADMLKCVRREYKPYFPQILNRTSQHLVVAFGV  250
ELKEMDSSGESYTLVSKLGLPSEGILSGDNALPKSGLLMSLLVVIFMNGN  300
CATEEEVWEFLGLLGIYDGILHSIYGDARKIITEDLVQDKYVVYRQVCNS  350
DPPCYEFLWGPRAYAETTKMRVLRVLADSSNTSPGLYPHLYEDALIDEVE  400
RALRLRA                                             407
```